REMARKS

It is respectfully submitted that the amendments submitted herewith function to add new claims 50-54 and to insert the sequence listing and appropriate sequence identifiers into the text of the present application to comply with 37 C.F.R. §1.821 to 1.825. These amendments are made without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents.

It is submitted that new claims 50-54 are in full compliance with the requirements of 35 U.S.C. §112. The amendments and remarks herein are not made for the purpose of patentability within the meaning of 35 U.S.C. §§ 101, 102, 103 or 112; but rather the amendments and remarks are made simply for clarification and to round out the scope of protection to which Applicants are entitled.

Support for the new claims is found throughout the specification, and may specifically be found in example 8 on pages 45-53.

It is respectfully asserted that the sequence disclosure contained in the application now fully complies with the requirements set forth in 37 C.F.R. § 1.821 to § 1.825.

It is respectfully submitted that the Sequence Listing conforms to the requirements of 37 C.F.R. §1.823(b). The Statements required by 37 C.F.R §1.821(f) and (g) are set forth below.

Pursuant to 37 C.F.R. §1.821 (g), the undersigned hereby states that this submission, filed in accordance with 37 C.F.R. §1.821 (g), does not contain new matter.

Pursuant to 37 C.F.R. §1.821 (f), the undersigned hereby states that the content of the paper and computer readable copies of the Sequence Listing submitted in accordance with 37 C.F.R. §1.821 (c) and (e), respectively, are the same.
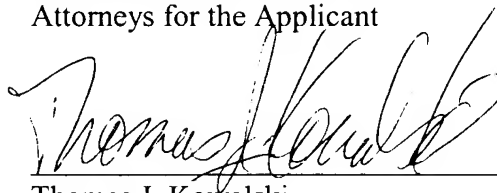
CONCLUSION

In view of the amendments, remarks and enclosures herein, it is respectfully submitted that the application now complies with all requirements set forth in the Notice. Accordingly, reconsideration and withdrawal of the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures ("Notice to Comply") is respectfully requested.

Respectfully submitted,

FROMMER LAWRENCE & HAUG LLP
Attorneys for the Applicant

By:

Thomas J. Kowalski
Reg. No. 32,147
(212) 588-0800

Enclosures: Paper and Diskette copies of Sequence Listing
Copy of Notice to Response To Notice To Comply
Return receipt postcard

"VERSION WITH MARKINGS TO SHOW CHANGES MADE"

Page 1, line 19:

The "strength" or "weakness" of doughs are [is] an important aspect of making farinaceous finished products from doughs, including baking. The "strength" or "weakness" of a dough is primarily determined by its content of protein and in particular the content and quality of the gluten protein is an important factor in that respect. Flours with a low protein content are [is]generally characterized as "weak." Thus, the cohesive, extensible, rubbery mass which is formed by mixing water and weak flour will usually be highly extensible when subjected to stress, but it will not return to its original dimensions when the stress is removed.

Page 28, line 32:

Table 3.1. Alignment of lipase 3 peptides with known lipase sequences

LIP_RHIDL (SEQ ID NO: 10)	MVSFISISQGVSLCLLVSSMMLGSSAVPVSGKSGSSNTAVSASDNAALPP	50
LIP_RHIMI (SEQ ID NO: 11)	MVLKQRANYLGFLIVFFTAFLV--EAVPIKRQSNSTVDS--------LLP	40
MDLA_PENCA (SEQ ID NO: 12)	MRLS-----------FFTAL-----------------SAVASLGYALPG	21
N-Terminal	**SVSTSTLDELQLFAQWSAAAYXSNN (SEQ ID NO: 20)**	

LIP_RHIDL	LISSRCAPPSNKGSKSDLQAEPYNMQKNTEWYESHGGNLTSIGKRDDNLV	100
LIP_RHIMI	LIPSRTSAPSSSPSTTDPEAPAM----------SRNGPLPS----DVETK	76
MDLA_PENCA	KLQSR------DVSTSELDQFEFWVQYAAASY-----------------	47
	.** . *... ..	

LIP_RHIDL	GGMTLDLPSDAPPISLSSSTNSASDGGKVVAATTAQIQEFTKYAGIAATA	150
LIP_RHIMI	YGMALNATSYPDSV------VQAMSIDGGIRAATSQEINELTYYTTLSANS	121
MDLA_PENCA	- -YEADYTAQVGDKL	60

LIP_RHIDL	YCRSVVPGNKWDCVQCQKWVPDGKIITTFT-SLLSDTNGYVLRSDKQKTI	199
LIP_RHIMI	YCRTVIPGATWDCIHCDA-TEDLKIIKTWS-TLIYDTNAMVARGDSEKTI	169
MDLA_PENCA	SCSKG- - - - - - -NCPEVEA - -TGATVSYDFSDSTITDTAGYIAVDHTNSAV	102

Page 29, line 4:

Peptide 1	**VHTGFWK (SEQ ID NO: 2)**
Peptide 2	**AWESAADELTSK (SEQ ID NO: 19)**

LIP_RHIDL	YLVFRGTNSFRSAITDIVFNFSDYKPVKGAKVHAGFLSSYEQVVNDYFPV	249
LIP_RHIMI	YIVFRGSSSIRNWIADLTFVPVSYPPVSGTKVHKGFLDSYGEVQNELVAT	219
MDLA_PENCA	VLAFRGSYSVRNWVADATFVHTNPGLCDGCLAELGFWSSWKLVRDDIIKE	152

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```
        . .***. * *.   . .*  .*     . .*  .. **...     .  ..
```

Peptide 2   **IK**

```
                    . .       . * .* . .*. ***** .* * *   . ** *.    .. .*  ..
```

LIP_RHIDL   VQEQLTAHPTYKVIVTGHSLGGAQALLAGMDLYQREPRLSPKNLSIFTVG   299
LIP_RHIMI   VLDQFKQYPSYKVAVTGHSLGGATALLCALDLYQREEGLSSSNLFLYTQG   269
MDLA_PENCA   LKEVVAQNPNYELVVVGHSLGAAVATLAATDL -- RGKGYPSAKLYAYA--   198

```
                    . .     . * .* . .*. ***** .* * *   . ** *.    .. .*  ..
```

LIP_RHIDL   GPRVGNPTFAYYVESTGPFQRTVHKRDIVPHVPPQSFGFLHPGESWIK   349
LIP_RHIMI   QPRVGDPAFANYVVSTGIPYRRTVNERDIVPHLPPAAFGFLHAGEEYWIT   319
MDLA-PENCA   SPRVGNAALAKYITAQGNNF-RFTHTNDPVPKLPLLSMGYVHVSPEYWIT   247

```
                    **** ... * *. .* . . * ....* **.. * ..*.. * .* **  .
```

LIP_RHIDL   SGTSN – V - - - - - QICTSEIETKDCSNSIVPFTSILD – HLSYF - DINEGSC   391
LIP_RHIMI   DNSPETV - - - - - QVCTSDLETSDCSNSIVPFTSVLD – HLSYF - GINTGLC   362
MDLA_PENCA   SPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHIWYFVQDAGKG   297

LIP_RHIDL   - - - - - - - L   392
LIP_RHIMI   - - - - - - - T   363
MDLA_PENCA   PGLPFKRV   305

Page 30, line 37:

Degenerated primers for PCR amplification of a fragment of the lipase gene were designed based on the amino acid sequence of the isolated peptides. The following three PCR primers were synthesized:

C035: TTC CAR YTN TTY GCN CAR TGG   (SEQ ID NO: 5)

18 mer 256 mixture, based on the N-terminal sequence QLFAQW. (SEQ ID NO: 21)

C037: GCV GCH SWY TCC CAV GC   (SEQ ID NO: 6)

17 mer 216 mixture, based on internal peptide 2 sequence AWESAA (reversed).(SEQ ID NO: 22)

Page 33, line 7:

Table 5.1. (SEQ ID NO: 13)PCR-generated putative *lipA* sequence

(The four amino acid fragments of table 5.1 are contained in SEQ ID NOS: 14-17)

```
              10          20          30          40          50          60
tacccgggntccattCAGTTGTTCGCGCAATGGTCTGCCGCAGCTTATTGCTCGAATA


              Q   L   F   A   Q   W   S   A   A   A   Y   C   S   N
              70          80          90         100         110         120


          ATATCGACTCGAAAGAVTCCAACTTGACATGCACGGCCAACGCCTGTCCATCAGTCGAGG
      N   I   D   S   K   X   S   N   L   T   C   T   A   N   A   C   P   S   V   E


              130         140         150         160         170         180
AGGCCAGTACCACGATGCTGCTGCTGGTGGAGTTCGACCTGTATGTCACTCAGATCGCAGACATAG
      E   A   S   T   T   M   L   L   E   F   D   L   Y   V   T   Q   I   A   D   I
              190         200         210         220         230         240
AGCACAGCTAATTGAACAGGACGAACGACTTTTGGAGGCACAGCCGGTTTCCTGGCCGCG
      E   H   S   -   L   N   R   T   N   D   F   W   R   H   S   R   F   P   G   R
              250         260         270         280         290         300
      G   Q   H   Q   Q   A   A   R   G   R   L   P   G   K   Q   H   D   -   E   L
              310         320         330
ATTGCTAATCYTGACTTCATCCTGGRAGATAACG
D   C   -   X   -   L   H   P   X   R   -   (SEQ ID NO: 13)
```

Page 37, line 10:

The gene was sequenced using cycle sequencing and conventional sequencing technology. The complete sequence (SEQ ID NO: [8] 18) is shown below in Table 6.1. The sequence has been determined for both strands for the complete coding region and about 100bp upstream and downstream of the coding region. The sequences downstream to the coding region have only been determined on one strand and [contains] contain a few uncertainties. In the sequence as shown below, the intron sequences are indicated as lowercase letters and the N-terminal and the two internal peptides (peptide 1 and peptide 2) are underlined:

Page 37, line 22:

Table 6.1. (SEQ ID NO: 18) The DNA sequence for the lipA gene and flanking sequences

```
   2   CCNDTTAATCCCCCACCGGGGTTCCCGCTCCCGGATGGAGATGGGGCCAAAACTGGCAAC
  61   CCCCAGTTGCGCAACGGAACAACCGCCGACCCGGAACAAAGGATGCGGATGAGGAGATAC
 121   GGTGCCTGATTGCATGGCTGGCTTCATCTGCTATCGTGACAGTGCTCTTTGGGTGAATAT
 181   TGTTGTCTGACTTACCCCGCTTCTTGCTTTTTCCCCCCTGAGGCCCTGATGGGGAATCGC
 241   GGTGGGTAATATGATATGGGTATAAAAGGGAGATCGGAGGTGCAGTTGGATTGAGGCAGT
 301   GTGTGTGTGTGCATTGCAGAAGCCCGTTGGTCGCAAGGTTTTGGTCGCCTCGATTGTTTG
 361   TATACCGCAAGATGTTCTCTGGACGGTTTGGAGTGCTTTTGACAGCGCTTGCTGCGCTGG
                  M  F  S  G  R  F  G  V  L  L  T  A  L  A  A  L
 421   GTGCTGCCGCGCCGGCACCGCTTGCTGTGCGGAgtaggtgtgcccgatgtgagatggttg
        G  A  A  A  P  A  P  L  A  V  R
 481   gatagcactgatgaagggtgaatagGTGTCTCGACTTCCACGTTGGATGAGTTGCAATTG
                              S  V  S  T  S  T  L  D  E  L  Q  L
 541   TTCGCGCAATGGTCTGCCGCAGCTTATTGCTCGAATAATATCGACTCGAAAGACTCCAAC
         F  A  Q  W  S  A  A  A  Y  C  S  N  N  I  D  S  K  D  S  N
 601   TTGACATGCACGGCCAACGCCTGTCCATCAGTCGAGGAGGCCAGTACCACGATGCTGCTG
        GAGTTCGACCTgtatgtcactcagatcgcagacatagagcacagctaatttgaacagGAC
        E  F  D  L                                                DAC
 722   GAACGACTTTGGAGGCACAGCCGGTTTCCTGGCCGCGGACAACACCAACAAGCGGCTCGT
        N  D  F  G  G  T  A  G  F  L  A  A  D  N  T  N  K  R  L  V
 782   GGTCGCCTTCCGGGGAAGCAGCACGATTGAGAACTGGATTGCTAATCTTGACTTCATCCT
        V  A  F  R  G  S  S  T  I  E  N  W  I  A  N  L  D  F  I  L
 842   GGAAGATAACGACGACCTCTGCACCGGCTGCAAGGTCCATACTGGTTTCTGGAAGGCATG
        E  D  N  D  D  L  C  T  G  C  K  V  H  T  G  F  W  K  A  W
 902   GGAGTCCGCTGCCGACGAACTGACGAGCAAGATCAAGTCTGCGATGAGCACGTATTCGGG
        E  S  A  A  D  E  L  T  S  K  I  K  S  A  M  S  T  Y  S  G
 962   CTATACCCTATACTTCACCGGGCACAGTTTGGGCGGCGCATTGGCTACGCTGGGAGCGAC
        Y  T  L  Y  F  T  G  H  S  L  G  G  A  L  A  T  L  G  A  T
1022   AGTTCTGCGAAATGACGGATATAGCGTTGAGCTGGTGAGTCCTTCACAAAGGTGATGGAG
        V  L  R  N  D  G  Y  S  V  E  L
1082   CGACAATCGGGAACAGACAGTCAATAGTACACCTATGGATGTCCTCGAATCGGAAACTAT
                            Y  T  Y  G  C  P  R  I  G  N  Y
1142   GCGCTGGCTGAGCATATCACCAGTCAGGGATCTGGGGCCAACTTCCGTGTTACACACTTG
        A  L  A  E  H  I  T  S  Q  G  S  G  A  N  F  R  V  T  H  L
1202   AACGACATCGTCCCCCGGGTGCCACCCATGGACTTTGGATTCAGTCAGCCAAGTCCGGAA
        N  D  I  V  P  R  V  P  P  M  D  F  G  F  S  Q  P  S  P  E
1262   TACTGGATCACCAGTGGCAATGGAGCCAGTGTCACGGCGTCGGATATCGAAGTCATCGAG
        Y  W  I  T  S  G  N  G  A  S  V  T  A  S  D  I  E  V  I  E
1322   GGAATCAATTCAACGGCGGGAAATGCAGGCGAAGCAACGGTGAGCGTTGTGGCTCACTTG
        G  I  N  S  T  A  G  N  A  G  E  A  T  V  S  V  V  A  H  L
1382   TGGTACTTTTTTGCGATTTCCGAGTGCCTGCTATAACTAGACCGACTGTCAGATTAGTGG
        W  Y  F  F  A  I  S  E  C  L  L  -
1442   ACGGGAGAAGTGTACATAAGTAATTAGTATATAATCAGAGCAACCCAGTGGTGGTGATGG
1502   TGGTGAAAGAAGAAACACATTGAGTTCCCATTACGKAGCAGWTAAAGCACKTKKGGAGGC
1562   GCTGGTTCCTCCACTTGGCAGTTGGCGGCCATCAATCATCTTTCCTCTCCTTACTTTCGT
1622   CCACCACAACTCCCATCCTGCCAGCTGTCGCATCCCCGGGTTGCAACAACTATCGCCTCC
1682   GGGGCCTCCGTGGTTCTCCTATATTATTCCATCCGACGGCCGACGTTTCACCCTCAACCT
1742   GCGCCGCCGCAAAATCTCCCCGAGTCGGTCAACTCCCTCGAACCGCCGCCCGCATCGACC
1802   TCACGACCCCGACCGTCTGYGATYGTCCAACCG
```

Page 39, line 1:

Table 6.2 Alignment of the lipase 3 sequence with known fungal lipases

LIPASE 3	MFSG - - - - - - - - - - - RFGVLL - TALAA	-15
MDLA_PENCA	MRLS - - - - - - - - - - FETAL - - - - - - - - - - - - - - - - - - SAVAS	-14
LIP_RHIDL	MVSFISISQGVSLCLLVSSMMLGSSAVPVSGKSGSSNTAVSADNAALPP	-50
LIP_RHIMI	MVLKQRANYLGFLIVFFTAFLV - - EAVPIKRQSNSTVDS- - - - - - - - - LPP	-40

LIPASE 3	L -	-16
MDLA_PENCA	L -	-15
LIP_RHIDL	LISSRCAPPSNKGSKSDLQAEPYNMQKNTEWYESHGGNLTSIGKRDDNLV	-100
LIP_RHIMI	LIPSRTSAPSSSPSTTDPEAPAM - - - - - - - - - - SRNGPLPS - - - - DVETK	-76

LIPASE 3	- - - - - - - - GAAAPAPLA- - - - - - - - - - -VRSVSTSTLDELQLFAQWSAAA	-47
MDLA_PENCA	- - - - - - - - GYALPGKLQ- - - - - - - - - - - - -SRDVSTSELDQFEFWVQYAAAS	-46
LIP_RHIDL	GGMTLDLPSDAPPISLSSSTNSASDGGKVVAATTAQIQEFTKYAGIAATA	-150
LIP_RHIMI	YGMALNATSYPDSV-----VQAMSIDGGIRAATSQEINELTYYTTLSANS	-121

LIPASE 3	YCSNNIDSK-DSNLTCTANACPSVEEASTTMLLEFDLTNDFGGTAGFLAA	-96
MDLA_PENCA	YYEADYTAQVGDKLSCSKGNCPEVEATGATVSYDFS-DSTITDTAGYIAV	-95
LIP_RHIDL	YCRSVVP---GNKWDCVQ—CQKWVPDGKIIT---TFTSLLSDTNGYVLR	-192
LIP_RHIMI	YCRTVIP---GATWDCIH—CDA-TEDLKIIK---TWSTLIYDTNAMVAR	-162

LIPASE 3	DNTNKRLVVAFRGSSTIENWIANLDFILEDNDDLCTGCKVHTGFWKAWES	-146
MDLA_PENCA	DHTNSAVVLAFRGSYSVRNWVADATFV-HTNPGLCDGCLAELGFWSSWKL	-144
LIP_RHIDL	SDKQKTIYLVFRGTNSFRSAITDIVFNFSDYKPV-KGAKVHAGFLSSYEQ	-241
LIP_RHIMI	GDSEKTIYIVFRGSSSIRNWIADLTFVPVSYPPV-SGTKVHKGFLDSYGE	-211

LIPASE 3	AADELTSKIKSAMSTYSGYTLYFTGHSLGGALATLGATVL—RNDGY-SV	-193
MDLA_PENCA	VRDDIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDL—RGKGYPSA	-192
LIP_RHIDL	VVNDYFPVVQEQLTAHPTYKVIVTGHSLGGAQALLAGMDLYQREPRLSPK	-291
LIP_RHIMI	VQNELVATVLDQFKQYPSYKVAVTGHSLGGATALLCALDLYQREEGLSSS	-261

LIPASE 3	ELYTY—GCPRIGNYALAEHITSQGSGANFRVTHLNDIVPRVPPMDFGFS	-241
MDLA_PENCA	KLYAY - - ASPRVGNAALAKYITAQGN - - NFRFTHTNDPVPKLPLLSMGYV	-238
LIP_RHIDL	NLSIFTVGGPRVGNPTFAYYVESTGIPFQ-RTVHKRDIVPHVPPQSFGFL	-340
LIP_RHIMI	NLFLYTQGQPRVGDPAFANYVVSTGIPYR-RTVNERDIVPHLPPAAFGFL	-310

LIPASE 3	QPSPEYWITSGNGASVTASDIEVIEGINSTAGNAGEATVSVV---AHLWY	-288
MDLA_PENCA	HVSPEYWITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHIWY	-288
LIP_RHIDL	HPGVESWIKSGTSN-VQICTSEIE------TKDCSNSIVPETSILDHLSY	-383
LIP_RHIMI	HAGEEYWITDNSPETVQVCTSDLE------TSDCSNSIVPFTSVLDHLSY	-354

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LIPASE 3	FFAISECL- - - - - - - -L	-297 (SEQ ID NO: 9)
MDLA_PENCA	FVQVDAGKGPGLPFKRV	-305 (SEQ ID NO: 12)
LIP_RHIDL	F - DINEGSC- - - - - - -L	-392 (SEQ ID NO: 10)
LIP_RHIMI	F - GINTGLC - - - - - - -T	-363 (SEQ ID NO: 11)

Page 40, line 31:

Table 6.3 Alignment of coding sequence of the *lipA* gene and gene coding for mono-diacyl lipase from *Penicillium camemberti*

```
LIPASE 3     MFSGRFGVLLTALAALGAAAPAPLAVRSVSTSTLDELQLFAQWSAAAYCS     -50
              |   |  |  |  |  || |  |  |  | ||| || |      |  || |
MDLA_PENCA   MRLSFFTAL - SAVASLGYALPGKLQSRDVSTSELDQFEFWVQYAAASYYE    -49


LIPASE 3     NN I DSK -- DSNLTCTANACPSVEEASTTMLLEFDLTNDFGGTAGFLAADNT    -99
               |   |    || ||   |       |        ||| | | |
MDLA_PENCA   ADYTAQVGDKLSCSKGNCPEVEATGATVSYDFS - DSTITDTAGY IAVDHT    -98


LIPASE 3     NKRLVVAFRGSSTIENW I ANLDFILEDNDDLCTGCKVHTGFWKAWESAAD    -149
              |    | ||| ||    || |   |    |   || ||   ||| |     |
MDLA_PENCA   NSAVVLAFRGSYSVRNWVADATFV-HTNPGLCDGCLAELGFWSSWKLVRD    -147


LIPASE 3     ELTSKIKSAMSTYSGYTLYFTGHSLGGALATLGATVLRNDGY-SVELYTY    -198
                 |         | |    ||||| | |||| || ||   || |   || |
MDLA_PENCA   DIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDLRGKGYPSAKLYAY    -197


LIPASE 3     GCPR IGNYALAEHITSQGSGANFRVTHLNDIVPRVPPMDFGFSQPSPEYW    -248
              ||   ||   |||    ||    |||  ||  ||  ||  |      ||||||| |
MDLA_PENCA   ASPRVGNAALAKYITAQGN- - NFRFTHTNDPVPKLPLLSMGYVHVSPEYW    -245


LIPASE 3     ITSGNGASVTASDIEVIEGINSTAGNAGEATVSVV - - - AHLWYFFAISEC    -295
              ||| |  |  |   ||| ||  |  |  || |           ||  |||
MDLA_PENCA   ITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDTFEAHIWYFVQVDAG    -295


LIPASE 3     L--------L -297 (SEQ ID NO: 9)
MDLA_PENCA   KGPGLPFKRV -305 (SEQ ID NO: 12)
```

Identity: 126 amino acids (42.42%)

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Page 41, line 30:

Table 6.4: Amino acid sequence of the precursor of lipase 3 (SEQ ID NO: 9)

```
              5        10       15        20       25        30
              |        |        |         |        |         |
    1    M F S G R F G V L L T A L A A L G A A A P A P L A V R S V S
   31    T S T L D E L Q L F A Q W S A A A Y C S N N I D S K D S N L
   61    T C T A N A C P S V E E A S T T M L L E F D L T N D F G G T
   91    A G F L A A D N T N K R L V V A F R G S S T I E N W I A N L
  121    D F I L E D N D D L C T G C K V H T G F W K A W E S A A D E
  151    L T S K I K S A M S T Y S G Y T L Y F T G H S L G G A L A T
  181    L G A T V L R N D G Y S V E L Y T Y G C P R I G N Y A L A E
  211    H I T S Q G S G A N F R V T H L N D I V P R V P P M D F G F
  241    S Q P S P E Y W I T S G N G A S V T A S D I E V I E G I N S
  271    T A G N A G E A T V S V V A H L W Y F F A I S E C L L
```

Number of residues: 297